

GenCore version 5.1.4.P5-4578  
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OM protein - protein search, using sw model

Run on: April 8, 2003, 14:25:27 ; Search time 75 Seconds  
(without alignments)  
968,288 Million cell updates/sec

Title: US-09-001-737-8  
Perfect score: 545  
Sequence: 1 MAKIEKFSADARAAMYRGVD.....TPAPAMPAGMDPGMMGG 545

Scoring table: GIGO  
Gapop 60.0 , Gapext: 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 8

Total number of hits satisfying chosen parameters: 350

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

1: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1980.DAT:\*

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3: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1983.DAT:\*

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20: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA2000.DAT:\*

21: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA2001.DAT:\*

22: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA2002.DAT:\*

23: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	545	100.0	545.	20	AYV3904
2	538	98.7	545	23	ABP28529
3	78	14.3	540	23	ABP28528
4	70	12.8	540	22	AAW10101
5	70	12.8	541	20	AYV23902
6	70	12.8	641	22	ABE1619
7	56	10.3	542	23	ABE23701
8	31	5.7	542	23	ABBA9241
9	26	4.8	539	20	AAV23916
10	4.4	2.2	224	20	AYV37100

11 24 Dihydrofolate reduc  
12 24 DHR/PolyPeptide B  
13 24 HypB protein. Chl  
14 24 C. psittaci1 HypB g  
15 24 Chlamydia pneumoniae  
16 24 Polypeptide B. Ch  
17 24 Amino acid sequenc  
18 24 Amino acid sequenc  
19 24 Chlamydophila pneumoniae  
20 24 Chlamydia pneumoniae  
21 24 Amino acid sequenc  
22 24 Dihydrofolate reduc  
23 24 DHR/PolyPeptide B  
24 24 Pseudomonas aerugi  
25 23 Propionibacterium  
26 23 S. epidermidis ope  
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Propionibacterium	Human EPH family T
Novel human diagno	
C. glutamicum SRT	
Arabidopsis thalia	
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Arabidopsis thalia	
C. glutamicum Prote	
C. glutamicum SRT	
Cantharis glabraea H	
Aspergillus fumiga	
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Candida glabrata H	
Histidine tagged C	
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Heat shock protein	
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Aspergillus fumiga	
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Peptide from libra	
Microbacterium sp. h	
Human ORFX ORF14	
Human ORFX protein	
Antigen from clust	
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Microbacterium sp. h	
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Hsp-65 peptide epi	
Heat shock protein	
peptide from libra	
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Microbacterium sp. h	
Microbacterium sp. h	

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232	2.0	22	21	AAW81995	305	9	1.7	558	ABB7885
233	1.1	2.0	20	AAW12294	306	8	1.5	9	ABB88282
234	1.1	2.0	104	AAW12293	307	8	1.5	9	AAE19467
235	1.1	2.0	114	AAW07688	308	8	1.5	9	AAE19467
236	1.1	2.0	114	AAW07689	309	8	1.5	13	AAW5696
237	1.1	2.0	114	AAW07690	310	8	1.5	15	AAW81623
238	1.1	2.0	114	AAW12292	311	8	1.5	15	AAW81621
239	1.1	2.0	118	AAW02075	312	8	1.5	15	AAW9847
240	1.1	2.0	120	AAW14877	313	8	1.5	15	AAW9874
241	1.1	2.0	120	AAW14883	314	8	1.5	15	AAW9874
242	1.1	2.0	135	AAW44098	315	8	1.5	15	AAW3525
243	1.1	2.0	145	AAW44097	316	8	1.5	15	AAW3525
244	1.1	2.0	156	AAW12291	317	8	1.5	15	AAW9455
245	1.1	2.0	177	AAW00869	318	8	1.5	15	AAW9455
246	1.1	2.0	212	AAW5326	319	8	1.5	15	AAW3553
247	1.1	2.0	247	AAW3519	320	8	1.5	15	AAW9784
248	1.1	2.0	252	AAW1357	321	8	1.5	15	AAW3462
249	1.1	2.0	258	AAW3109	322	8	1.5	26	AAW3309
250	1.1	2.0	281	AAW02079	323	8	1.5	72	AAW3002
251	1.1	2.0	342	AAW14356	324	8	1.5	93	ABB01535
252	1.1	2.0	397	AAW5326	325	8	1.5	122	ABB0141
253	1.1	2.0	412	AAW9547	326	8	1.5	134	AAW13001
254	1.1	2.0	423	AAW5325	327	8	1.5	156	AAW9773
255	1.1	2.0	433	AAW49136	328	8	1.5	244	AAW3364
256	1.1	2.0	446	AAW50252	329	8	1.5	246	AAW60028
257	1.1	2.0	459	AAW02077	330	8	1.5	246	AAW5922
258	1.1	2.0	464	AAW5673	331	8	1.5	256	AAW67775
259	1.1	2.0	469	AAW49135	332	8	1.5	287	AAU6503
260	1.1	2.0	477	AAW1772	333	8	1.5	387	AAU6503
261	1.1	2.0	477	AAW50259	334	8	1.5	364	AAW53962
262	1.1	2.0	536	AAW49134	335	8	1.5	440	AAW0061
263	1.1	2.0	541	AAW50251	336	8	1.5	524	AAW91959
264	1.1	2.0	568	AAW12924	337	8	1.5	533	AAW65988
265	1.1	2.0	586	AAW1771	338	8	1.5	545	AAW67798
266	1.1	2.0	586	AAW50258	339	8	1.5	546	AAW67798
267	1.1	2.0	611	AAW19770	340	8	1.5	546	AAW67798
268	1.1	2.0	611	AAW50257	341	8	1.5	548	AAW67797
269	1.1	2.0	648	AAW59450	342	8	1.5	549	AAW67799
270	1.1	2.0	650	AAW50250	343	8	1.5	552	AAW67798
271	1.1	2.0	650	AAW8269	344	8	1.5	1106	AAU6502
272	1.1	2.0	650	AAW8290	345	8	1.5	1191	AAU6501
273	1.1	2.0	650	AAW19770	346	8	1.5	1195	AAU6501
274	1.1	2.0	651	AAW50257	347	8	1.5	1325	AAU6049
275	1.1	2.0	651	AAW50257	348	8	1.5	1422	ABB02345
276	1.1	2.0	650	AAW94826	349	8	1.5	1504	ABB0358
277	1.1	2.0	650	AAW19770	350	8	1.5	1795	ABB62094
278	1.1	2.0	650	AAW19770					
279	1.1	2.0	650	AAW19770					
280	1.1	2.0	650	AAW19770					
281	1.1	2.0	650	AAW19770					
282	1.1	2.0	650	AAW19770					
283	1.1	2.0	650	AAW19770					
284	1.1	2.0	650	AAW19770					
285	1.1	2.0	650	AAW19770					
286	1.1	2.0	650	AAW19770					
287	1.1	2.0	650	AAW19770					
288	1.1	2.0	650	AAW19770					
289	1.1	2.0	650	AAW19770					
290	1.1	2.0	650	AAW19770					
291	1.1	2.0	650	AAW19770					
292	1.1	2.0	650	AAW19770					
293	1.1	2.0	650	AAW19770					
294	1.1	2.0	650	AAW19770					
295	1.1	2.0	650	AAW19770					
296	1.1	2.0	650	AAW19770					
297	1.1	2.0	650	AAW19770					
298	1.1	2.0	650	AAW19770					
299	1.1	2.0	650	AAW19770					
300	1.1	2.0	650	AAW19770					
301	1.1	2.0	650	AAW19770					
302	1.1	2.0	650	AAW19770					
303	1.1	2.0	650	AAW19770					
304	1.1	2.0	650	AAW19770					
305	1.1	2.0	650	AAW19770					
306	1.1	2.0	650	AAW19770					
307	1.1	2.0	650	AAW19770					
308	1.1	2.0	650	AAW19770					
309	1.1	2.0	650	AAW19770					
310	1.1	2.0	650	AAW19770					
311	1.1	2.0	650	AAW19770					
312	1.1	2.0	650	AAW19770					
313	1.1	2.0	650	AAW19770					
314	1.1	2.0	650	AAW19770					
315	1.1	2.0	650	AAW19770					
316	1.1	2.0	650	AAW19770					
317	1.1	2.0	650	AAW19770					
318	1.1	2.0	650	AAW19770					
319	1.1	2.0	650	AAW19770					
320	1.1	2.0	650	AAW19770					
321	1.1	2.0	650	AAW19770					
322	1.1	2.0	650	AAW19770					
323	1.1	2.0	650	AAW19770					
324	1.1	2.0	650	AAW19770					
325	1.1	2.0	650	AAW19770					
326	1.1	2.0	650	AAW19770					
327	1.1	2.0	650	AAW19770					
328	1.1	2.0	650	AAW19770					
329	1.1	2.0	650	AAW19770					
330	1.1	2.0	650	AAW19770					
331	1.1	2.0	650	AAW19770					
332	1.1	2.0	650	AAW19770					
333	1.1	2.0	650	AAW19770					
334	1.1	2.0	650	AAW19770					
335	1.1	2.0	650	AAW19770					
336	1.1	2.0	650	AAW19770					
337	1.1	2.0	650	AAW19770					
338	1.1	2.0	650	AAW19770					
339	1.1	2.0	650	AAW19770					
340	1.1	2.0	650	AAW19770					
341	1.1	2.0	650	AAW19770					
342	1.1	2.0	650	AAW19770					
343	1.1	2.0	650	AAW19770					
344	1.1	2.0	650	AAW19770					
345	1.1	2.0	650	AAW19770					
346	1.1	2.0	650	AAW19770					
347	1.1	2.0	650	AAW19770					
348	1.1	2.0	650	AAW19770					
349	1.1	2.0	650	AAW19770					
350	1.1	2.0	650	AAW19770					
351	1.1	2.0	650	AAW19770					
352	1.1	2.0	650	AAW19770					
353	1.1	2.0	650	AAW19770					
354	1.1	2.0	650	AAW19770					
355	1.1	2.0	650	AAW19770					
356	1.1	2.0	650	AAW19770					
357	1.1	2.0	650	AAW19770					
358	1.1	2.0	650	AAW19770					
359	1.1	2.0	650	AAW19770					
360	1.1	2.0	650	AAW19770					
361	1.1	2.0	650	AAW19770					
362	1.1	2.0	650	AAW19770					
363	1.1	2.0	650	AAW19770					
364	1.1	2.0	650	AAW19770					
365	1.1	2.0	650	AAW19770					
366	1.1	2.0	650	AAW19770					
367	1.1	2.0	650	AAW19770					
368	1.1	2.0	650	AAW19770					
369	1.1	2.0	650	AAW19770					
370	1.1	2.0	650	AAW19770					
371	1.1	2.0	650	AAW19770					
372	1.1	2.0	650	AAW19770					
373	1.1	2.0	650	AAW19770					
374	1.1	2.0	650	AAW19770					
375	1.1	2.0	650	AAW19770					
376	1.1	2.0	650	AAW19770					
377	1.1	2.0	650	AAW19770					
378	1.1	2.0	650	AAW19770					
379	1.1	2.0	650	AAW19770					
380	1.1	2.0	650	AAW19770					
381	1.1	2.0	650	AAW19770					
382	1.1	2.0	650	AAW19770					
383	1.1	2.0	650	AAW19770					
384	1.1	2.0	650	AAW19770					
385	1.1	2.0	650	AAW19770					
386	1.1	2.0	650	AAW19770					
387	1.1	2.0	650	AAW19770					
388	1.1	2.0	650	AAW19770					
389	1.1	2.0	650	AAW19770					
390	1.1	2.0	650	AAW19770					
391	1.1	2.0	650	AAW19770					
392	1.1	2.0	650	AAW19770					

XX  
PR 31-DEC-1997; 97US-0001737.  
XX  
(STRE-) STRESSGEN BIOTECHNOLOGIES CORP.  
XX  
PI Mizzen L, Wisniewski J;  
DR WPI: 1999-43039736.  
XX  
N-PSDB; AXB6155.

PT New nucleic acid encoding heat shock protein-60 from *Streptococcus*,  
PT useful in vaccines, as carriers for other immunogens, as anticancer  
agents and for diagnosis  
XX  
PS Claim 11; Fig 4A-B; 176pp; English.

XX  
CC The present sequence represents a heat shock protein, designated Hsp60-2.  
CC The protein, its fragments, variants and fusion proteins, are  
used to elicit or enhance an immune response against *Streptococcus*,  
CC and to elicit a similar response to a target antigen fused to the  
CC protein. Unlike other immunological carriers, Hsp60 proteins are not  
CC immunosuppressive so provide an increased response to any conjugated or  
CC fused antigen. Also, where used for cancer control, they lack the side  
CC effects associated with endotoxins. They can also be used to detect  
CC specific antibodies and in treatment or prevention of tumours  
(e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or  
CC liver). The Hsp60 polynucleotide is used for recombinant production  
CC of the protein, as a source of primers and probes for detecting and  
CC streptococci in standard hybridization/amplification assays, and  
CC therapeutically in gene therapy vectors.  
XX  
SQ Sequence 545 AA;

Query Match 100.0%; Score 545; DB 20; Length 545;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKEIKFSNDARAAVGRGVDMLADTVKVLGPKGRNVYLEAKFGSPPLITNDGVTIAKIE 60  
DB 1 LEDRHENNGAKLVSEVASKTNDIAGDTTATVLTQAIHVHGLKNVTAGANPIGIRGIE 60  
DB 61 LEDRHENNGAKLVSEVASKTNDIAGDTTATVLTQAIHVHGLKNVTAGANPIGIRGIE 120  
DB 61 LEDRHENNGAKLVSEVASKTNDIAGDTTATVLTQAIHVHGLKNVTAGANPIGIRGIE 120  
QY 121 TATTAVERKATAQPSGKREIAKQVAASSSERKQEKYSEAMERVGNDGVITIERSG 180  
DB 121 TATTAVERKATAQPSGKREIAKQVAASSSERKQEKYSEAMERVGNDGVITIERSG 180  
QY 181 METTLEVEVGEGMDFREYLSQYMWYDNEKAVADLENPLILDKKNIODILPLERVLK 240  
DB 181 METTLEVEVGEGMDFREYLSQYMWYDNEKAVADLENPLILDKKNIODILPLERVLK 240  
QY 241 TNRPLLIADDYDGEALPTVLNKRITFENVAVKAPGFDRRKAMLDIAITGGVIT 300  
DB 241 TNRPLLIADDYDGEALPTVLNKRITFENVAVKAPGFDRRKAMLDIAITGGVIT 300  
QY 301 EDIGLELKDATMTAQKMTIDSVWVGGSSSEANRNLALNSOLENTSPDR 360  
DB 301 EDIGLELKDATMTAQKMTIDSVWVGGSSSEANRNLALNSOLENTSPDR 360  
QY 361 EKQERLAKLAGVAVIKGAPETALKEMKIERDAALNTRADEVGIVAGGTALIV 420  
DB 361 EKQERLAKLAGVAVIKGAPETALKEMKIERDAALNTRADEVGIVAGGTALIV 420  
QY 421 IERVAALELEGDDTRGTRNVLRALEPVRQALNAGYEGSVWIDKLNSPAGTGFNATG 480  
DB 421 IERVAALELEGDDTRGTRNVLRALEPVRQALNAGYEGSVWIDKLNSPAGTGFNATG 480  
QY 481 EWMDDMITGIDPWPVTRSLQMASVASLILTEVWANKPERATPAPMAGMDPGMM 540  
DB 481 EWMDDMITGIDPWPVTRSLQMASVASLILTEVWANKPERATPAPMAGMDPGMM 540  
SQ Sequence 545 AA;

Query Match 98.7%; Score 538; DB 23; Length 545;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IKFSDARAAMVGRGVDMLADTVKVLGPKGRNVYLEAKFGSPPLITNDGVTIAKIELEDH 64  
DB 7 IKFSDARAAMVGRGVDMLADTVKVLGPKGRNVYLEAKFGSPPLITNDGVTIAKIELEDH 66

QY 65 FERNMGAKLVSSEVASKTNIDTAGDGTATVLTQAVIHEGLKNTVAGANPIGIRGIRETATA 124  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 67 FENMGAKLVSSEVASKTNIDTAGDGTATVLTQAVIHEGLKNTVAGANPIGIRGIRETATA 126  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 125 TAVEALKAIQPVSKRSEATAQAVAVASSERSEKVEYISEAMERVGNDVITERSRGME 184  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 127 TAVEALKAIQPVSKRSEATAQAVAVASSERSEKVEYISEAMERVGNDVITERSRGME 186  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 185 LEVVERQDFGYSQWYMDNSMADLENFILTDKVKSNQDIPPLBLVLTQAVIHEGLKNTVAGANPIGIRGIRETATA 244  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 187 LEVVERQDFGYSQWYMDNSMADLENFILTDKVKSNQDIPPLBLVLTQAVIHEGLKNTVAGANPIGIRGIRETATA 246  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 245 LLIADDDGEGALPLVLUKIRGTVENYAVAPGRDRRKAMLDIAITGGVITBDLG 304  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 247 LLIADDDGEGALPLVLUKIRGTVENYAVAPGRDRRKAMLDIAITGGVITBDLG 306  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 305 LELKDNTMTALGQAKITVKDSTVTEGSESSEATANRITALIKSQLTTSDPDKLQ 364  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 307 LELKDNTMTALGQAKITVKDSTVTEGSESSEATANRITALIKSQLTTSDPDKLQ 366  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 365 ERLAKILAGGAVIKVGAPETALKEMMLRIDALNATRAAVEEVAGGTLITYEVK 424  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 367 ERLAKILAGGAVIKVGAPETALKEMMLRIDALNATRAAVEEVAGGTLITYEVK 426  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 425 AALELEGGDDATGGRNVLRALEEVVROALNQYEVSVVIDLKNSPAGTGFNATEBWD 484  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 427 AALELEGGDDATGGRNVLRALEEVVROALNQYEVSVVIDLKNSPAGTGFNATEBWD 486  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 QY 485 MIKTGIDPVKVTRSLONAASVASLILTEAVVANKPERATPAPAMPGMDPGMMGG 542  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 487 MIKTGIDPVKVTRSLONAASVASLILTEAVVANKPERATPAPAMPGMDPGMMGG 544  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 RESULT 3  
 ARB28528  
 ID ARB28528 standard; Protein; 540. AA.  
 AC ARB20528;  
 XX  
 DT 02-JUL-2002 (first entry)  
 DE Streptococcus polypeptide SEQ ID NO 6232.  
 XX  
 KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KW group A streptococcus; Streptococcus; progenes; antibacterial; gene therapy.  
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
 OS Streptococcus agalactiae.  
 PN WO200234771-A2.  
 XX  
 PD 02-MAY-2002.  
 XX  
 PF 29-OCT-2001; 2001WO-GB04789.  
 XX  
 PR 27-OCT-2000; 2000GB-0026333.  
 PR 24-NOV-2000; 2000GB-0028727.  
 PR 07-MAR-2001; 2001GB-0005640.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 PT Telford J, Malignani V, Margarit Ros YI, Grandi G, Fraser C;  
 PT Tellelin H  
 XX  
 DR WPI; 2002-35236/38.  
 DR N-PSDE; ABN69159.  
 XX  
 PT New Streptococcus protein for the treatment or prevention of infection  
 PT or disease caused by Streptococcus bacteria, such as meningitis, and  
 PT for detecting a compound that binds to the protein -  
 XX

PS Claim 1; Page 3785; 4525PP; English.  
 XX  
 CC The invention relates to a protein (ARB25413-ARB30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 543 sequences (S1), given in the specific composition. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ARB604 AN7126 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins.  
 CC Sequence 540 AA:  
 Query Match 14.3%; Score 78; DB 23; Length 540;  
 Best Local Similarity 100.0%; Prod. No. Je-66;  
 Matches 78; Conservative 0; Mismatches 0; Gaps 0;  
 Indels 0;  
 DE CPE 104 protein sequence.  
 XX  
 KW Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CPE; CEG; Conserved Essential Gene; bacterial infection; antisense therapy; antibiotic resistance.  
 KW OS Streptococcus pneumoniae.  
 PN WO200149721-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 29-DEC-2000; 2000WO-US35604.  
 PR 30-DEC-1999; 99US-0174089.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Dougherty TJ, Pucci MJ, Dougherty BA, Davison DB, Brucolari RE;  
 PI Thanassi JA;  
 XX  
 DR WPI; 2001-46671/54.  
 DR N-PSDB; AAH0800.  
 XX  
 PT Nucleic acids encoding conserved essential genes involved in bacterial replication which are potential targets for the treatment of antibiotic resistant bacterial infections -  
 XX  
 PS Claim 27; Pages 356-358; 380pp; English.

CC The present invention relates to nucleic acids (AM90701-AM90918),  
 CC encoding polypeptides (AM01002-AM0114), which are essential for the  
 CC viability of a bacterial cell wall. The acronym CEG stands for "CEG For  
 CC Expression", where CEG stands for "Conserved Essential Gene". The nucleic  
 acids are useful for detecting the presence of proteins essential for the  
 CC viability of a bacterial cell wall in samples such as cells, tissues,  
 CC biological fluids, blood, serum, nose, ear or throat swabs with ligands,  
 CC and for detecting corresponding target nucleic acid molecules with  
 CC complementary sequences. The nucleic acids are also useful for  
 CC determining whether a genomic nucleotide sequence of interest is  
 CC essential for viability of a bacterial cell or whether it resides within a  
 CC portion of an open reading frame of the genomic sequence of interest  
 CC (comprising 200-500 base pairs) into the genomic sequence of interest  
 CC which confers a selectable phenotype to the cell, and determining cell  
 CC viability with a selectable agent such as chloramphenicol. The nucleic acids  
 CC also enable identification of targets suitable for the treatment of  
 CC antibiotic resistant bacterial infections.

SQ sequence 540 AA;

Query Match 12.8%; Score 70; DB 22; Length 540;  
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 242 NRPLIILADDVGEALPLTVINKRGTENVAVAKPGCFGDRRKAMLDIALITGGVITE 301  
 Db 242 NRPLIILADDVGEALPLTVINKRGTENVAVAKPGCFGDRRKAMLDIALITGGVITE 301

Oy 302 DLGELKDAT 311  
 Db 302 DLGELKDAT 311

RESULT 5

ID AAY23902  
 ID AAY23902 standard; Protein: 541 AA.

AC AAY23902;  
 DT 22-SEP-1999 (first entry)

XX Streptococcus pneumoniae heat shock protein (Hsp)60-2.

DE Heat shock protein; Hsp60-2; immune response; immunological carrier;  
 KW cancer control; tumour; sarcoma; cancer; gene therapy.

OS Streptococcus pneumoniae.

XX WO935270-A1.

XX PD 15-JUL-1999.

XX PP 29-DEC-1998; 98WO-CA01203.

XX PR 31-DEC-1997; 97US-0001737.

XX PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

PI Mizzen L, Wisniewski J;

XX DR WPI: 1999-430397/35.

DR N-PSDB; AAX8613.

PT New nucleic acid encoding heat shock protein-60 from Streptococcus,  
 PT useful in vaccines as carriers for other immunogens, as anticancer  
 agents and for diagnosis.

XX PS Claim 11; Fig 2A-B; 17pp; English.

CC The present sequence represents a heat shock protein, designated Hsp60-2.

CC The protein, its fragments, variants and fusion proteins, are  
 CC used to elicit or enhance an immune response against Streptococcus,  
 CC and to elicit a similar response to a target antigen fused to the  
 CC protein. Unlike other immunological carriers, Hsp60 proteins are not  
 CC immunosuppressive so provide an increased response to any conjugated or  
 CC fused antigen. Also, where used for cancer control, they lack the side  
 CC effects associated with endotoxins. They can also be used to detect  
 CC specific antibodies and in treatment or prevention of tumours  
 (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or  
 CC liver). The Hsp60 polynucleotide is used for recombinant production  
 CC of the protein, as a source of primers and probes for detecting  
 CC streptococci in standard hybridization/amplification assays, and  
 CC therapeutically in gene therapy vectors.

SQ Sequence 541 AA;

Query Match 12.8%; Score 70; DB 20; Length 541;  
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 242 NRPLIILADDVGEALPLTVINKRGTENVAVAKPGCFGDRRKAMLDIALITGGVITE 301  
 Db 242 NRPLIILADDVGEALPLTVINKRGTENVAVAKPGCFGDRRKAMLDIALITGGVITE 301

Oy 302 DLGELKDAT 311  
 Db 302 DLGELKDAT 311

RESULT 6

ID AAB31619  
 ID AAB31619 standard; Protein: 641 AA.

AC AAB31619;

DT 30-APR-2001 (first entry)

DE Amino acid sequence of Hsp65-B7 fusion protein.

XX KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;  
 KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;  
 KW E7 protein.

OS Synthetic.

OS Streptococcus pneumoniae.

OS Human papillomavirus.

XX PN WO200104344-A2.

XX PD 18-JAN-2001.

XX PF 10-JUL-2000; 2000WO-US18828.

XX PR 08-JUL-1999; 99US-0143757.

XX PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX PI Siegel M, Chu NR, Mizzen LA;

XX DR WPI: 2001-138361/14.

XX DR N-PSDB; AAF25036.

PT Screening for compounds that stimulate Th1-like responses in CD4+ T  
 PT lymphocyte cells.

XX PS Example 15; Fig 15A-B; 88pp; English.

CC The present sequence represents a fusion protein comprising a  
 CC Streptococcus pneumoniae heat shock protein (Hsp) 65 fused to a HSV16 E7  
 CC protein. The fusion protein is used in the method of the invention. The  
 CC specification describes a method of determining whether a compound  
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T  
 CC lymphocyte cells. The method comprises contacting naive lymphocytes

in vitro with a fusion protein comprising at least a fragment of Hsp65, and then detecting the TLR-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate TLR-like responses in response to microbial pathogens.

XX SQ sequence 641 AA:

RESULT 7

Query Match 12.8%; Score 70; DB 22; Length 641;  
Best Local Similarity 100.0%; Pred. No. 1.9e-58; Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ID ABB53701; AC ABB53701; DE ABB53701; DT 05-FEB-2002 (first entry); PR 11-APR-2000; PN WO20017735-A2.

ABB53701 standard; Protein; 542 AA.

QY 242 NRPLLIADDVDEGEALPTLVNLRKIGTFPNVVAVKAPGFCDRRKAMLEDAITLGGVITE 301  
Db 242 NRPLLIADDVDEGEALPTLVNLRKIGTFPNVVAVKAPGFCDRRKAMLEDAITLGGVITE 301  
Qy 302 DIGLELKDT 311  
Db 302 DIGLELKDT 311

RESULT 8

Query Match 12.8%; Score 70; DB 22; Length 641;  
Best Local Similarity 100.0%; Pred. No. 1.9e-58; Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ID ABB49241; AC ABB49241; DE Listeria monocytogenes protein #1945; DT 05-FEB-2002 (first entry); PR 11-APR-2000; PN WO20017735-A2.

ABB49241 standard; Protein; 542 AA.

QY 44 GSPLITNDGVTAKETELEDIFHENNGAKLYSEVASKNTNDIAGDTTATVLTQIV 99  
Db 44 GSPLITNDGVTAKETELEDIFHENNGAKLYSEVASKNTNDIAGDTTATVLTQIV 99

XX SQ sequence 542 AA:

PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; PI Daniels J, Goebel W, Kieft J, Kuhn M, Ng B, Vazquez-Boland JA; PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; PI Madueno E, De Pablo B, Weiland J, Kaerst U, Entian K, Hauf J; PI Rose M, Voss H; XX DR WPI; 2002-010914/01.

XX DR WPI; 2002-010914/01.

XX PR Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment and prevention of *Listeria* and related bacterial infections, and related polypeptides -

XX PR Claim 6; SEQ ID No 1946; 192pp; French.

XX PS The present invention relates to the genome sequence of *Listeria monocytogenes* EGD-e (see AB03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in *L. monocytogenes* and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of *L. monocytogenes* and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate *L. monocytogenes*-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by *L. monocytogenes* and related organisms.

XX Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [http://www.wipo.int/pdb/published\\_pct\\_sequences](http://www.wipo.int/pdb/published_pct_sequences).

XX Sequence 542 AA:





50 Sequence 544 AA;  
 Query Match 4.4%; Score 24; DB 12; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-14; Mismatches 0; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 273 AVKAPGFGDRRKAMMEDIALTGG 296  
 Db 275 AVKAPGFGDRRKAMMEDIALTGG 298

RESULT 14  
 AAR67383  
 ID AAR67383 standard; Protein: 544 AA.  
 XX  
 AC AAR67383;  
 XX  
 DT 22-JUN-1995 (first entry)  
 XX  
 C. psittaci HypB gene product.  
 XX  
 Urease; immunogen; vaccine; diagnostic; heat shock protein; HSP;  
 KW GroEL-like protein; Helicobacter felis.  
 XX  
 OS Chlamydia psittaci.  
 XX  
 PN WO94265001-A.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PF 19-MAY-1994; 94WO-EP01625.  
 XX  
 PR 19-MAY-1993; 93EP-0401309.  
 PR 19-NOV-1993; 93WO-EP03259.  
 XX  
 PA (INRM ) INST NAT SANTE & RECH MEDICALE.  
 PA (INSP ) INST PASTEUR.  
 XX  
 PI Ferrero R, Labigne A, Suerbaum S, Thibierge J;  
 XX  
 DR WPI, 1995-006797/01.  
 XX  
 PT DNA from Helicobacter pylori and Helicobacter felis - used to  
 PT develop prods. for detection, treatment and prevention of  
 PT Helicobacter infection.  
 XX  
 PS Disclosure: Fig. 7A(i-vii); 168pp; English.

XX  
 CC The sequence of the Helicobacter pylori heat shock protein A  
 CC (given in AAR67374) was compared to that of other GroEL-like  
 CC proteins from Legionella pneumophila (AAR67381), Escherichia coli  
 CC (AAR67382), Chlamydia psittaci (AAR67383), Mycobacterium leprae  
 CC (AAR67384), human mitochondrial protein Pi (AAR67385), and regions  
 XX  
 Sequence 544 AA;

XX  
 PS Sequence 544 AA;  
 XX  
 PT The sequence of the Helicobacter pylori heat shock protein A  
 PT (given in AAR67374) was compared to that of other GroEL-like  
 PT proteins from Legionella pneumophila (AAR67381), Escherichia coli  
 PT (AAR67382), Chlamydia psittaci (AAR67383), Mycobacterium leprae  
 PT (AAR67384), human mitochondrial protein Pi (AAR67385), and regions  
 XX  
 Sequence 544 AA;

XX  
 Query Match 4.4%; Score 24; DB 16; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-14; Mismatches 0; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 273 AVKAPGFGDRRKAMMEDIALTGG 296  
 Db 275 AVKAPGFGDRRKAMMEDIALTGG 298

RESULT 15  
 AAW10975  
 ID AAW10975 standard; Protein: 544 AA.  
 XX  
 AC AAW10975;  
 XX  
 DT 21-MAY-1997 (first entry)

XX Chlamydia pneumoniae antigen used as DHFR-linked fusion protein.  
 DE  
 XX DHFR; dihydrofolate reductase; Chlamydia pneumoniae; pneumonia;  
 KW antibody production; diagnosis; fusion protein.  
 XX OS Chlamydia pneumoniae.  
 XX  
 FT KEY Location/Qualifiers  
 FT Misc-difference 25 /note= "given as Gle in three letter amino  
 acid code in the specification"  
 FT  
 XX PR JP08294391-A.  
 XX PD 12-NOV-1996.  
 XX PF 28-APR-1995; 95JP-0106007.  
 XX PR 28-APR-1995; 95JP-0106007.  
 XX PA (HITB ) HITACHI CHEM CO LTD.  
 XX DR WPI; 1997-036901/04.  
 XX  
 PT Fusion protein comprising di-hydro-folate reductase and Chlamydia  
 PT pneumoniae antigen useful in prodn. of C. pneumoniae antibodies  
 PT for diagnosis of infection.  
 XX PS Claim 1: Page 11-12; 17pp; Japanese.  
 XX CC AAW10974 encodes a 544 residue Chlamydia pneumoniae antigen, at least  
 CC 5 contiguous amino acids of which are fused to a dihydrofolate  
 CC reductase (DHFR) enzyme. Fusion proteins produced are useful for the  
 CC production of anti-C. pneumoniae antibodies which are useful for the  
 CC diagnosis and treatment of infectious diseases caused by C. pneumoniae.  
 XX SQ Sequence 544 AA;  
 XX  
 PS Sequence 544 AA;  
 XX  
 PT Query Match 4.4%; Score 24; DB 18; Length 544;  
 PT Best Local Similarity 100.0%; Pred. No. 3.7e-14; Mismatches 0; Indels 0; Gaps 0;  
 PT Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PT  
 Qy 273 AVKAPGFGDRRKAMMEDIALTGG 296  
 Db 275 AVKAPGFGDRRKAMMEDIALTGG 298

XX  
 Search completed: April 8, 2003, 14:35:09  
 Job time : 81 secs